Two pmol of primer were used.

Pmol Promoter-primer			RLU
RP modified	CO modified	Unmodifed	
0	15	0.1	450,157
2	13	0	678,871
5	10	0.01	681,647
5	10	0	755,839

M1 This example shows that a mixture of unmodified and modified or a mixture of different types of modified promoter-primers amplified well, allowing detection of 3 tmol of RNA target in one hour.

IN THE CLAIMS:

Please cancel claims 76, 77, 85, 87 and 91 without prejudice.

Kindly substitute the following claims:

M2 39. (Four Times Amended) A kit for amplifying *Mycobacterial* nucleic acid, said kit containing:

a first oligonucleotide comprising the nucleotide base sequence of xGCCGTCACCCCACCAACAAGCT (SEQ ID NO: 22); and

a second oligonucleotide comprising the nucleotide base sequence of xGGGATAAGCCTGGGAAACTGGGTCTAATACC (SEQ ID NO: 2),

wherein x is nothing or is a sequence recognized by an RNA polymerase, and wherein each said oligonucleotide is from 22 to about 100 bases in length.

40. (Four Times Amended) An oligonucleotide of from 22 to about 100 bases in length and comprising the nucleotide base sequence of xGCCGTCACCCCACCAACAAGCT

(SEQ ID NO: 22) or the sequence perfectly complementary thereto, wherein x is nothing or is a sequence recognized by an RNA polymerase.

41. (Five Times Amended) A kit for amplifying and detecting *Mycobacterial* nucleic acid, said kit containing:

a first oligonucleotide of from 24 to about 100 bases in length and comprising the nucleotide base sequence of SEQ ID NO: 3; and

a second oligonucleotide of from 22 to about 100 bases in length and comprising a nucleotide base sequence selected from the group consisting of xGCCGTCACCCCACCAACAAGCT (SEQ ID NO: 22) and xGGGATAAGCCTGGGAAACTGGGTCTAATACC (SEQ ID NO: 2), wherein x is nothing or is a sequence recognized by an RNA polymerase.

42. (Five Times Amended) A kit for amplifying and detecting *Mycobacterial* nucleic acid, said kit containing:

a first oligonucleotide of from 23 to about 100 bases in length and comprising the nucleotide base sequence of SEQ ID NO: 8; and

a second oligonucleotide of from 20 to about 100 bases in length and comprising a nucleotide base sequence selected from the group consisting of xCCAGGCCACTTCCGCTAACC (SEQ ID NO: 23) and xCGCGGAACAGGCTAAACCGCACGC (SEQ ID NO: 7), wherein x is nothing or is a sequence recognized by an RNA polymerase.

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48. (Three Times Amended) The kit of claim 41, wherein said second oligonucleotide has a 3' end which is modified to reduce or block extension of said second oligonucleotide by a polymerase.

49. (Three Times Amended) The kit of claim 48 further comprising a third oligonucleotide having a 3' end which is unmodified, wherein said third oligonucleotide is from 20 to about 100 bases in length and comprises a nucleotide base sequence selected from the group consisting of xCCAGGCCACTTCCGCTAACC (SEQ ID NO: 23) and xCGCGGAACAGGCTAAACCGCACGC (SEQ ID NO: 7), wherein x is nothing or is a sequence recognized by an RNA polymerase, and wherein the nucleotide base sequences of said second and third oligonucleotides are different.

50. (Three Times Amended) The oligonucleotide of claim 40, wherein said oligonucleotide has a 3' end which is modified to reduce or block extension of said oligonucleotide by a polymerase.

51. (Four Times Amended) A composition comprising:

a first oligonucleotide in accordance with said oligonucleotide of claim 40, wherein said first oligonucleotide has a 3' end which is not modified to reduce or block extension of said first oligonucleotide by a polymerase; and

a second oligonucleotide in accordance with said oligonucleotide of claim 40, wherein said second oligonucleotide has a 3' end which is modified to reduce or block extension of said second oligonucleotide by a polymerase.

54. (Four Times Amended) The composition of claim 51 further comprising a third oligonucleotide having a 3' end which is modified to reduce or block extension by a polymerase, wherein the 3' ends of said second and third oligonucleotides are differently modified.

55. (Three Times Amended) The kit of claim 42, wherein said second oligonucleotide has a 3' end which is modified to reduce or block extension of said second oligonucleotide by a polymerase.

56. (Three Times Amended) The kit of claim 55 further comprising a third oligonucleotide having a 3' end which is not modified to reduce or block extension of said third oligonucleotide by a polymerase.

67. (Three Times Amended) A primer oligonucleotide of from 10 to 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 22 or the sequence perfectly complementary thereto.

68. (Twice Amended) The primer oligonucleotide of claim 67, said primer being from 15 to 50 nucleotide bases in length.

69. (Twice Amended) The primer oligonucleotide of claim 67, said primer oligonucleotide comprising the nucleotide base sequence of SEQ ID NO: 22 or the sequence perfectly complementary thereto.

70. (Three Times Amended) The primer oligonucleotide of claim 67, wherein the nucleotide base sequence of said primer oligonucleotide consists of or is contained within the nucleotide base sequence of SEQ ID NO: 22 or the sequence perfectly complementary thereto.

71. (Twice Amended) The primer oligonucleotide of claim 67 further comprising a nucleotide base sequence which is recognized by an RNA polymerase which initiates transcription.

72. (Three Times Amended) The primer oligonucleotide of claim 71, said primer oligonucleotide comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO: 1 and SEQ ID NO: 19.

M8 cancel

73. (Three Times Amended) The primer oligonucleotide of claim 71, wherein the nucleotide base sequence of said primer oligonucleotide consists of or is contained within a nucleotide base sequence selected from the group consisting of SEQ ID NO: 1 and SEQ ID NO: 19.

M9

SUB N6

75. (Three Times Amended) A composition for amplification of *Mycobacterium tuberculosis* nucleic acid, said composition comprising:

a first primer oligonucleotide consisting of an oligonucleotide of from 10 to 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO:23 or the sequence perfectly complementary thereto; and

a second primer oligonucleotide consisting of an oligonucleotide of from about 10 to about 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 7 or the sequence perfectly complementary thereto.

M10

78. (Three Times Amended) The composition of claim 75, wherein at least one of said first and second primer oligonucleotides further comprises a nucleotide base sequence which is recognized by an RNA polymerase which initiates transcription.

SUB N7

79. (Four Times Amended) The composition of claim 75 further comprising a hybridization probe of from about 10 to about 100 nucleotide bases in length which hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid to form a detectable duplex under reaction conditions, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 8 or the sequence perfectly complementary thereto.

M11 Sub. N8

80. (Twice Amended) The composition of claim 79, wherein said probe comprises a nucleotide base sequence selected from the group consisting of SEQ ID NO: 8 and the sequence perfectly complementary thereto.

M12

82. (Three Times Amended) The composition of claim 79, wherein said probe further comprises a detectable label.

M13

83. (Amended) The composition of claim 82, wherein said detectable label is an acridinium ester.

M14 Sub N9

84. (Three Times Amended) A composition for amplification of *Mycobacterium tuberculosis* nucleic acid, said composition comprising first and second primer oligonucleotides, each of said primer oligonucleotides being from about 10 to about 100 nucleotide bases in length,

wherein said first primer oligonucleotide hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, and wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 22 or the sequence perfectly complementary thereto, and

wherein said second primer oligonucleotide hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, and wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 2 or the sequence perfectly complementary thereto.

M15 Sub 03

86. (Twice Amended) The composition of claim 84, wherein said first primer oligonucleotide comprises the nucleotide base sequence of SEQ ID NO: 22, and wherein said second primer oligonucleotide comprises the nucleotide base sequence of SEQ ID NO: 2.

M16 88. (Twice Amended) The composition of claim 84 or 86, wherein at least one of said first and second primer oligonucleotides further comprises a nucleotide base sequence which is recognized by an RNA polymerase which initiates transcription.

Sub N10 89. (Twice Amended) The composition of claim 84 or 86 further comprising a hybridization probe of from about 10 to about 100 nucleotide bases in length which hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region of *Mycobacterium tuberculosis* nucleic acid to form a detectable duplex under reaction conditions, wherein said region consists of the nucleotide base sequence of SEQ ID NO: 3 or the sequence perfectly complementary thereto.

M17 Sub N11 90. (Amended) The composition of claim 89, wherein said probe comprises the nucleotide base sequence of SEQ ID NO: 3 or the sequence perfectly complementary thereto.

M18 92. (Amended) The composition of claim 89, wherein said probe comprises a detectable label.

M19 Sub N12 96. (Twice Amended) A probe mix comprising:

a hybridization probe of from 10 to 100 nucleotide bases in length which hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid to form a detectable hybridization duplex under reaction conditions, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 8 or the sequence perfectly complementary thereto; and

a helper oligonucleotide.

M20

97. (Amended) The probe mix of claim 96, wherein said helper oligonucleotide consists essentially of a nucleic acid sequence selected from the group consisting of SEQ ID NO: 9 and SEQ ID NO: 10.

98. (Amended) A probe mix comprising:

SUB N13

a hybridization probe of from 10 to 100 nucleotide bases in length which hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid to form a detectable hybridization duplex under reaction conditions, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 3 or the sequence perfectly complementary thereto; and

a helper oligonucleotide.

99. (Amended) The probe mix of claim 98, wherein said helper oligonucleotide consists essentially of a nucleic acid sequence selected from the group consisting of SEQ ID NO: 4 and SEQ ID NO: 5.

SUB N14

100. (Three Times Amended) A kit for amplifying *Mycobacterial* nucleic acid, said kit containing:

a first oligonucleotide comprising xCCAGGCCACTTCCGCTAACC (SEQ ID NO: 23); and

M21

a second oligonucleotide comprising xCGCGGAACAGGCTAAACCGCACGC (SEQ ID NO: 7),

wherein x is nothing or is a sequence recognized by an RNA polymerase.

101. (Three Times Amended) A composition useful in the detection of *Mycobacterium tuberculosis*, said composition comprising:

a) a hybridization probe of from about 10 to about 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region of a target *Mycobacterium tuberculosis* nucleic acid, wherein the nucleotide base sequence of said region is a nucleotide base sequence selected from the group consisting SEQ ID NO: 3, SEQ ID NO: 8, and the sequences perfectly complementary thereto; and

b) a primer oligonucleotide of from about 10 to about 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region of *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is a nucleotide base sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 7, SEQ ID NO: 22, SEQ ID NO: 23, and the sequences perfectly complementary thereto.

M21 cont'd

102. (Amended) A composition comprising:

M22

a first oligonucleotide comprising a first primer sequence able to hybridize at or near the 3' end of a (+) target nucleic acid sequence, a 5' promoter sequence, and a modification at or near the 3' end of said first primer sequence which reduces or blocks extension of said first primer sequence by a polymerase compared to said first primer sequence not having said modification;

a second oligonucleotide comprising a second primer sequence able to hybridize at or near the 3' end of said (+) target sequence, a 5' promoter sequence, and an optionally present modification at or near the 3' end of said second primer sequence which reduces or blocks extension of said second primer sequence by a polymerase compared to said second primer sequence not having said modification, wherein said second oligonucleotide hybridizes to said (+) target sequence in effectively the same position as said first oligonucleotide, and wherein said modification to said second primer sequence, if present, is different than said modification to said first primer sequence;

a third oligonucleotide comprising a third primer sequence able to hybridize to the 3' end of a (-) target nucleic acid sequence which is the complement of said (+) target sequence, an optionally present 5' promoter sequence, and an optionally present modification at or near the 3' end

of said third primer sequence which reduces or blocks extension of said third primer sequence by a polymerase compared to said third primer sequence not having said modification;

an enzyme selected from the group consisting of a DNA-dependent DNA polymerase and an RNA-dependent DNA polymerase; and

M22 Cont'd

one or more RNA polymerases that recognize said promoter sequence of said first and second oligonucleotides.

M23

108. (Amended) The composition of claim 102 further comprising a molecule selected from the group consisting of DMSO, dimethylformamide, ethylene glycol, zinc and glycerol.

109. (Amended) The composition of claim 102 further comprising a helper oligonucleotide.

M24

111. (Amended) The composition of claim 102, wherein said second primer sequence comprises said modification at or near its 3' end.

112. (Amended) The composition of claim 111 further comprising a fourth oligonucleotide comprising a fourth primer sequence that hybridizes in effectively the same position as said first and second oligonucleotides and an optionally present 5' promoter sequence, wherein said fourth primer sequence does not contain a modification at or near its 3' end which reduces or blocks extension of said fourth primer sequence.

113. (Amended) The composition of claim 111, wherein the 3' end modifications to said first and second primer sequences are independently selected from the group consisting of an alkane diol modification, a 3' deoxynucleotide residue, a nucleotide with a nonphosphodiester linkage, a non-nucleotide modification, a base non-complementary to said target sequence, and a dideoxynucleotide.

114. (Amended) The composition of claim 111, wherein the 3' end modifications to said first and second primer sequences are independently selected from the group consisting of cordycepin, a ribonucleotide, and a phosphorothioate nucleotide.

115. (Amended) The composition of claim 102, wherein said third primer sequence does not comprise said modification at or near its 3' end.

116. (Amended) The composition of claim 102, wherein said third oligonucleotide comprises said 5' promoter sequence.

117. (Amended) The composition of claim 116, wherein said third primer sequence comprises said modification at or near its 3' end.

118. (Amended) The composition of claim 102, wherein said first and second primer sequences are the same.

119. (Amended) The composition of claim 102, wherein said first and second primer sequences are different.

120. (Amended) A composition comprising:

a first oligonucleotide comprising a first primer sequence able to hybridize to the 3' end of a (+) target nucleic acid sequence, an optionally present 5' promoter sequence, and an optionally present modification at or near the 3' end of said first primer sequence which reduces or blocks extension of said first primer sequence by a polymerase compared to said first primer sequence not having said modification;

M24

a second oligonucleotide comprising a second primer sequence able to hybridize at or near the 3' end of a (-) target nucleic acid sequence which is the complement of said (+) target

sequence, a 5' promoter sequence, and a modification at or near the 3' end of said second primer sequence which reduces or blocks extension of said second primer sequence by a polymerase compared to said second primer sequence not having said modification;

a third oligonucleotide comprising a third primer sequence able to hybridize at or near the 3' end of said (-) target sequence, a 5' promoter sequence, and an optionally present modification at or near the 3' end of said third primer sequence which reduces or blocks extension of said third primer sequence by a polymerase compared to said third primer sequence not having said modification, wherein said third oligonucleotide hybridizes to said (-) target sequence in effectively the same position as said second oligonucleotide, and wherein said modification to said third oligonucleotide, if present, is different than said modification to said second oligonucleotide;

an enzyme selected from the group consisting of DNA-dependent DNA polymerase and RNA-dependent DNA polymerase; and

one or more RNA polymerases that recognize said promoter sequences of said first and second oligonucleotides.

M24 Cont

M25

126. (Amended) The composition of claim 120 further comprising a molecule selected from the group consisting of DMSO, dimethylformamide, ethylene glycol, zinc and glycerol.

127. (Amended) The composition of claim 120 further comprising a helper oligonucleotide.

M26

129. (Amended) The composition of claim 120, wherein said third primer sequence comprises said modification at its 3' end.

130. (Amended) The composition of claim 129 further comprising a fourth oligonucleotide comprising a fourth primer sequence that hybridizes in effectively the same position as said second and third oligonucleotides and an optionally present 5' promoter sequence, wherein

said fourth primer sequence does not comprise a modification at or near its 3' end which reduces or blocks primer extension of said fourth primer sequence.

131. (Amended) The composition of claim 129, wherein said 3' end modifications to said second and third primer sequences are independently selected from the group consisting of an alkane diol modification, a 3' deoxynucleotide residue, a nucleotide with a nonphosphodiester linkage, a non-nucleotide modification, a base non-complementary to said target sequence, and a dideoxynucleotide.

132. (Amended) The composition of claim 129, wherein the 3' end modifications to said second and third primer sequences are independently selected from the group consisting of cordycepin, a ribonucleotide, and a phosphorothioate nucleotide.

133. (Amended) The composition of claim 120, wherein said first primer sequence does not comprise said modification at or near its 3' end.

134. (Amended) The composition of claim 120, wherein said first oligonucleotide comprises said 5' promoter sequence.

135. (Amended) The composition of claim 120, wherein said first primer sequence comprises said modification at or near its 3' end.

136. (Amended) The composition of claim 134, wherein said promoter sequences of said first, second and third oligonucleotides are the same.

M26

137. (Amended) The composition of claim 120, wherein said promoter sequences of said second and third primer sequences are the same.

138. (Amended) The composition of claim 120, wherein said promoter sequences of said second and said third primer sequences are different.

139. (Amended) A kit comprising:

a first oligonucleotide comprising a first primer sequence able to hybridize at or near the 3' end of a (+) target nucleic acid sequence, a 5' promoter sequence, and a modification at or near the 3' end of said first primer sequence which reduces or blocks extension of said first primer sequence by a polymerase compared to said first primer sequence not having said modification;

a second oligonucleotide comprising a second primer sequence able to hybridize at or near the 3' end of said (+) target sequence, a 5' promoter sequence, and an optionally present modification at or near the 3' end of said second primer sequence which reduces or blocks extension of said second primer sequence by a polymerase compared to said second primer sequence not having said modification, wherein said second oligonucleotide hybridizes to said (+) target sequence in effectively the same position as said first oligonucleotide, and wherein said modification to said second primer sequence, if present, is different than said modification to said first primer sequence;

a third oligonucleotide comprising a third primer sequence able to hybridize to the 3' end of a (-) target nucleic acid sequence which is the complement of said (+) target sequence, an optionally present 5' promoter sequence, and an optionally present modification at or near the 3' end of said third primer sequence which reduces or blocks extension of said third primer sequence by a polymerase compared to said third primer sequence not having said modification;

an enzyme selected from the group consisting of DNA-dependent DNA polymerase and RNA-dependent DNA polymerase; and

one or more RNA polymerases that recognize said promoter sequences of said first and second oligonucleotides.

M26

140. (Amended) The kit of claim 139 further comprising a hybridization probe able to indicate the presence of said (+) target sequence or said (-) target sequence.

141. (Amended) A kit comprising:

a first oligonucleotide comprising a first primer sequence able to hybridize to the 3' end of a (+) target nucleic acid sequence, an optionally present 5' promoter sequence, and an optionally present modification at or near the 3' end of said first primer sequence which reduces or blocks extension of said first primer sequence by a polymerase compared to said first primer sequence not having said modification;

a second oligonucleotide comprising a second primer sequence able to hybridize at or near the 3' end of a (-) target nucleic acid sequence which is the complement of said (+) target sequence, a 5' promoter sequence, and a modification at or near the 3' end of said second primer sequence which reduces or blocks extension of said second primer sequence by a polymerase compared to said second primer sequence not having said modification;

a third oligonucleotide comprising a third primer sequence able to hybridize at or near the 3' end of said (-) target sequence, a 5' promoter sequence, and an optionally present modification at or near the 3' end of said third primer sequence which reduces or blocks extension of said third primer sequence by a polymerase compared to said third primer sequence not having said modification, wherein said third oligonucleotide hybridizes to said (-) target sequence in effectively the same position as said second oligonucleotide and said modification to said third oligonucleotide, if present, is different than said modification to said second oligonucleotide;

an enzyme selected from the group consisting of DNA-dependent DNA polymerase and RNA-dependent DNA polymerase; and

one or more RNA polymerases that recognize said promoter sequences of said first and second oligonucleotides.

M26 Cont

142. (Amended) The kit of claim 141 further comprising a hybridization probe able to indicate the presence of said (+) target sequence or said (-) target sequence.

M27 SUB N15

143. (Twice Amended) An oligonucleotide of from 20 to about 100 bases in length, said oligonucleotide comprising a nucleotide base sequence selected from the group consisting of xCCAGGCCACTTCCGCTAACC (SEQ ID NO: 23), xCGCGGAACAGGCTAAACCGCACGC (SEQ ID NO: 7), and the sequences perfectly complementary thereto, wherein x is nothing or a sequence recognized by an RNA polymerase.

144. (Twice Amended) The composition of claim 143, wherein said oligonucleotide has a 3' end which is modified to reduce or block extension of said oligonucleotide by a polymerase.

SUB N16

145. (Twice Amended) A composition comprising:

a first oligonucleotide in accordance with said oligonucleotide of claim 143, wherein said first oligonucleotide has a 3' end which is not modified to reduce or block extension of said first oligonucleotide by a polymerase; and

a second oligonucleotide in accordance with said oligonucleotide of claim 143, wherein said second oligonucleotide has a 3' end which is modified to reduce or block extension of said second oligonucleotide by a polymerase.

146. (Twice Amended) The composition of claim 145 further comprising a third oligonucleotide having a 3' end which is modified to reduce or block extension of said third oligonucleotide by a polymerase, wherein the 3' ends of said second and third oligonucleotides are differently modified.

SUB N17

147. (Twice Amended) A primer oligonucleotide of from 10 to 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base

sequence of said region is the nucleotide base sequence of SEQ ID NO: 23 or the sequence perfectly complementary thereto.

148. (Amended) The primer oligonucleotide of claim 147, wherein said primer oligonucleotide is from 15 to 50 nucleotide bases in length.

149. (Amended) The primer oligonucleotide of claim 147, wherein said primer oligonucleotide is from about 20 to about 100 nucleotide bases in length.

SUB N18

150. (Amended) The primer oligonucleotide of claim 69, wherein said primer oligonucleotide is from 22 to about 100 nucleotide bases in length.

151. (Twice Amended) The primer oligonucleotide of claim 147, wherein said primer oligonucleotide comprises the nucleotide base sequence of SEQ ID NO: 23 or the sequence perfectly complementary thereto.

152. (Twice Amended) The primer oligonucleotide of claim 147, wherein the nucleotide base sequence of said primer oligonucleotide consists of or is contained within the nucleotide base sequence of SEQ ID NO: 23 or the sequence perfectly complementary thereto.

153. (Amended) The primer oligonucleotide of claim 147 further comprising a nucleotide base sequence which is recognized by an RNA polymerase which initiates transcription.

M27

154. (Amended) The primer oligonucleotide of claim 153, wherein said primer oligonucleotide comprises the nucleotide base sequence of SEQ ID NO: 6 or SEQ ID NO: 19.

155. (Amended) The primer oligonucleotide of claim 153, wherein the nucleotide base sequence of said primer oligonucleotide consists of or is contained within the nucleotide base sequence of SEQ ID NO: 6 or SEQ ID NO: 19.

156. (Amended) The composition of claim 82 further comprising:

a first helper oligonucleotide comprising the nucleotide base sequence of SEQ ID NO: 9; and

a second helper oligonucleotide comprising the nucleotide base sequence of SEQ ID NO: 10.

157. (Amended) The composition of claim 101 further comprising a helper oligonucleotide comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 9, SEQ ID NO: 10, and the sequences perfectly complementary thereto.

Sub M19

158. (Amended) A kit comprising a primer oligonucleotide of from about 10 to about 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region of *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is a nucleotide base sequence selected from the group consisting of SEQ ID NO: 7, SEQ ID NO: 22, SEQ ID NO: 23, and the sequences perfectly complementary thereto.

159. (Amended) A composition comprising a specifically detectable nucleic acid hybrid formed under reaction conditions between a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid, or a sequence perfectly complementary thereto, and a hybridization probe of from about 10 to about 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of said region, or the

M27

sequence perfectly complementary thereto, wherein the nucleotide base sequence of said region is a nucleotide base sequence selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 8, and the RNA equivalents thereof.

160. (Amended) A composition useful in the detection of *Mycobacterium tuberculosis*, said composition comprising:

a) a hybridization probe of from about 10 to about 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under reaction conditions, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 3 or the sequence perfectly complementary thereto; and

b) a primer oligonucleotide of from about 10 to about 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is selected from the group consisting of SEQ ID NO: 22, SEQ ID NO: 2, and sequences perfectly complementary thereto.

161. (Amended) The composition of claim 160 further comprising a helper oligonucleotide comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO: 4, SEQ ID NO: 5, and the sequences perfectly complementary thereto.

162. (Amended) A kit comprising a primer oligonucleotide of from about 10 to about 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 22 or the sequence perfectly complementary thereto.

M27

163. (Amended) A composition comprising a specifically detectable nucleic acid hybrid formed under reaction conditions between a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid, or a sequence perfectly complementary thereto, and a hybridization probe of from about 10 to about 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of said region, or the sequence perfectly complementary thereto, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 3 or the RNA equivalent thereof.

164. (Amended) A composition useful in the detection of *Mycobacterium tuberculosis*, said composition comprising:

a) a hybridization probe of from about 10 to about 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under reaction conditions, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 8 or the sequence perfectly complementary thereto; and

b) a primer oligonucleotide of from about 10 to about 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is a nucleotide base sequence selected from the group consisting of SEQ ID NO: 23, SEQ ID NO: 7, and the sequences perfectly complementary thereto.

165. (Amended) The composition of claim 164 further comprising a helper oligonucleotide comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 10, and the sequences perfectly complementary thereto.

M27

166. (Amended) A kit comprising a primer oligonucleotide of from about 10 to about 100 nucleotide bases in length which hybridizes to a nucleotide base sequence region present

in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said region is a nucleotide base sequence selected from the group consisting of SEQ ID NO: 23, SEQ ID NO: 7, and the sequences perfectly complementary thereto.

167. (Amended) A composition comprising a specifically detectable nucleic acid hybrid formed under reaction conditions between a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid, or a sequence perfectly complementary thereto, and a hybridization probe of from about 10 to about 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of said region, or the sequence perfectly complementary thereto, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 8 or the RNA equivalent thereof.

168. (Amended) The kit of claim 41 further comprising a helper oligonucleotide comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO: 4, SEQ ID NO: 5, and the sequences perfectly complementary thereto.

M27 Cancel

169. (Amended) The kit of claim 42 further comprising a helper oligonucleotide comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 10, and the sequences perfectly complementary thereto.

M28

170. (Amended) The composition of claim 80, wherein said probe further comprises a detectable label.

171. (Amended) The composition of claim 170, wherein said detectable label is an acridinium ester.

172. (Amended) The composition of claim 170 further comprising:

a first helper oligonucleotide comprising the nucleotide base sequence of SEQ ID NO: 9; and

a second helper oligonucleotide comprising the nucleotide base sequence of SEQ ID NO: 10.

173. (New) The kit of claim 162 further comprising a second primer oligonucleotide of from about 10 to about 100 nucleotide bases in length which hybridizes to a second nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under amplification reaction conditions, wherein the nucleotide base sequence of said second region is the nucleotide base sequence of SEQ ID NO: 2 or the sequence perfectly complementary thereto.

174. (New) The kit of claim 166, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 23 or the sequence perfectly complementary thereto.

175. (New) The kit of claim 166, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 7 or the sequence perfectly complementary thereto.

176. (New) A hybridization probe of from about 10 to about 100 nucleotide bases in length comprising a nucleotide base sequence which hybridizes with specificity to at least 10 contiguous bases of a nucleotide base sequence region present in *Mycobacterium tuberculosis* nucleic acid under reaction conditions, wherein the nucleotide base sequence of said region is the nucleotide base sequence of SEQ ID NO: 3 or the sequence perfectly complementary thereto.